IGF system on the adaptation to grazing after TMR feeding during early lactation. During the first 60 d postpartum (DPP), cows were assigned to 1) TMR (30 kgDM/d offered; 45% forage, 55% concentrate) and 2) 50% pasture in one (am) grazing session (6 h; pasture allowance 4 cm above ground level = 15 kgDM/d) + 50% TMR (15 kgDM/d offered) (G1). At 61 DPP and during 21 d, all cows were managed as G1 group determining 2 treatments (TREAT): PostTMR and G1. Plasma and liver biopsies were collected pre (+55 DPP) and post (+75 DPP) dietary change. Gene expression was quantified by SYBR-Green real time RT-PCR. Means from a repeated analysis using a mixed model were considered to differ when $P < 0.05$. Average milk energy output and BCS from 61 to 82 DPP did not differ between TREAT (27.5 and 25.7 ± 1.4 Mcal/d and 2.8 and 2.7 ± 0.1 units for PostTMR and G1, respectively). Plasma IGF1 concentrations at +75 DPP were greater in PostTMR than G1 cows (161 vs. 127 ± 26 ng/mL) as decreased from +55 at +75 DPP only in the latter cows. Plasma insulin and leptin as well as hepatic IGF1, IGF2 IGFBP2, and IGFBP4 mRNA were not affected by TREAT, DPP or its interaction. Before the diet change (+55 DPP), PostTMR cows had greater hepatic IGFBP1 mRNA but lower IGFBP3 mRNA than G1 cows. However, IGFBP1 mRNA had a 2.1-fold decrease while IGFBP3, IGFBP5 and IGFBP6 mRNA had 0.4 to 0.9-fold increase in PostTMR cows with the dietary change (+55 to +75 DPP). In addition, hepatic IGFBP3 mRNA decreased by 65% during this period in G1 cows. These changes determined that at +75 DPP, hepatic IGFBP3, IGFBP5 and IGFBP6 mRNA were greater while IGFBP1 mRNA was less in PostTMR than G1 cows. Decreased plasma IGF1 and hepatic IGFBP3 mRNA in G1 cows were associated with the increased milk yield from +55 to +75 DPP in these cows. In addition, while milk yield, BCS, and plasma IGF1 were maintained after the diet change in PostTMR cows, expression of IGFBP mRNA in the liver was modified in these cows

Key Words: nutrition, gene expression, grazing

W429 Effects of feeding 3-nitrooxypropanol (NOP) on rumen microbial profiles in lactating dairy cows and beef cattle. Mi Zhou*[1], Yanhong Chen[1], Jennifer Haisan[1], Atmir Romero-Perez[1,2], Karen A. Beauchemin[2], Masahito Oba[1], Maik Kindermann[3], Stephane Duval[4], and Le Luo Guan[1], *[1]Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada, [3]DSM Nutritional Products, Animal Nutrition & Health, Basel, Switzerland, [4]DSM Nutritional Products France, Research Centre for Animal Nutrition and Health, Saint Louis Cedex, France.*

3-Nitrooxypropanol (NOP) can reduce CH_4 production from the rumen of dairy cows and beef cattle, but the effect of NOP on the rumen microbiome is unknown. The current project aimed to evaluate the microbial profile changes in 4 studies with NOP fed to beef and dairy cows. Rumen contents were collected from 2 dairy (Study 1: Haisan et al., 2014; Study 2: unpublished data) and 2 beef (Study 3: Romero-Perez et al., 2014; Study 4: Romero-Perez et al., 2015) studies, and subjected to genomic DNA extraction. Bacterial, archaeal and protozoal rRNA fragments were amplified and subjected to pyrosequencing analysis using 454 Titanium FLX (Roche). The main bacteria phyla in the rumen were found to be affected by NOP treatments: in dairy, Firmicutes was greater in control than in NOP dairy cows for Study 1 (58 vs 55%, $P = 0.03$); while in beef, Bacteroidetes proportions varied among different NOP levels for Study 3 (from 31% for Control to 36% for NOP, $P < 0.01$) and among NOP treatment periods for Study 4 ($P = 0.04$). NOP also influenced other minor bacterial phyla, with the magnitude of impact differing among studies. The major methanogen genera were similar for all studies, and similar trends were found for both beef and dairy studies: *Methanobrevibacter ruminanitum* was greater ($P < 0.05$) in all 4 studies (57 vs 46%; 66 vs 51%; 52 vs 37%; 30 vs 20%) while *Mbb. gottschalkii* was less ($P < 0.01$) in cattle receiving NOP (Studies 2 to 4: 36 vs 20%; 59 vs 42%; 68 vs 54%). *Mbb. smithii* and *Methanosphaera stadtmanae* responded to NOP feeding in different ways depending upon the study. Entodiniomorphida predominated the protozoal community (>90%). The protozoa composition was not affected by NOP, and no clusters formed according to NOP dosage. In conclusion, NOP may reduce enteric CH_4 though changing rumen microbial community, but its effect of each phylotype was different, requiring further experimentation to understand its mode of action in altering the rumen microbiome.

Key Words: 3-nitrooxypropanol, rumen microbiome

W430 Effect of protein supplementation to low-quality forage diets on enteric methane production and ruminal microbial community structure of beef steers. Adam L. Shreck*[1], Nirosh D. Aluthge[3], Jenny S. Jennings[2], Samodha C. Fernando[3], and N. Andy Cole[1], *[1]USDA-ARS, Bushland, TX, [2]Texas Agrilife Research, Amarillo, TX, [3]University of Nebraska-Lincoln, Lincoln, NE.*

British-cross steers (n = 23; initial BW: 344 ± 33.9 kg) were used in a 3-period crossover design to evaluate the effect of protein supplementation to low-quality forage on ruminal methane (CH_4) and metabolic carbon dioxide (CO_2) emissions, forage intake, and microbial composition. Steers were individually given ad libitum access to low-quality bluestem hay (3.9% crude protein) and provided one of 3 supplements: (dry matter basis): no protein (CON), cottonseed meal (CSM; 0.29% of body weight (BW) daily) or dried distillers grains with solubles (DDGS; 0.41% of BW daily). Ruminal CH_4 and metabolic CO_2 fluxes were obtained 6.3 ± 1.6 times/steer daily using a GreenFeed unit (C-Lock Inc., Rapid City, SD). Microbial community structure of ruminal fluid collected using stomach tubes was determined using 16S rRNA based sequencing. Forage intake increased ($P < 0.01$) by 35.0% with protein supplementation; however, no difference ($P = 0.14$; SEM: 0.36) was observed between CSM (5.82 kg/d) and DDGS (5.50 kg/d). Flux of CO_2 (g/d) was greater ($P < 0.01$; SEM: 172.0) for steers fed CSM (5,520) and DDGS (5,453) than for steers fed CON (4,895). Steers supplemented with CSM (204.9) had greater ($P < 0.01$; SEM: 5.8) CH_4 emissions (g/d) than DDGS (189.2), both of which were greater ($P < 0.01$) than CON (174.1). Methane emissions, as a proportion of GE intake (Y_m), were lower ($P < 0.01$; SEM: 0.25) for DDGS (7.27%) and CSM steers (7.80%) than CON (10.10%). Principal coordinate analysis revealed shifts in microbial community structure with CON having greater abundance of specific operational taxonomic units (OTU) classified as *Firmicutes* and *Streptococcus* while CSM contained greater *Bacteroidetes* and *Prevotella* and DDGS steers had greater abundance of specific OTUs belonging to *Clostridiales* and *Anaerobiviro*. Results of this study suggests that the common practice of supplementing protein to cattle consuming low-quality forage increases overall gas emissions but yields beneficial decreases in greenhouse gas emissions per unit of intake and alters microbial community structure.

Key Words: enteric methane, protein, 16S rRNA

W431 Effect of a *Saccharomyces cerevisiae* preparation on in vitro ruminal fermentation of four fibrous substrates. Karla Y. Valdés[1], Iván Mateos[1], Cristina Saro[1], Alexey Díaz[1,4], María Dolores Carro[2], Abdelfattah Z. M. Salem[3], and María José Ranilla*[1,4], *[1]Animal Production Department, University of León, León, Spain, [2]Agriculture Production Department, Technical University of Madrid, Madrid, Spain, [3]Faculty of Veterinary Medicine and Animal Science,*

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Yeast cultures, especially *Saccharomyces cerevisiae*, are beneficial in the rumen, and have been progressively introduced into the feed industry. They can affect microbial activities, thus improving fiber digestion, modifying VFA production and increasing animal performance. Most of studies have focused on yeast effects when good quality and high concentrate diets are used, but much less attention has been paid to the possible effects with fibrous feeds. In this study, the effects of a preparation of *S. cerevisiae* (strain SC-47) on in vitro ruminal fermentation of 4 fibrous feeds differing in quality and chemical composition were analyzed. Two low-quality forages (barley straw and *Pennisetum purpureum* clon Cuba CT-115) and 2 medium-quality forages (alfalfa hay and grass hay) were used. Samples of the forages (500 mg) were accurately weighed into 120-mL serum bottles, and incubated with buffered rumen fluid (50 mL) at 39°C for 24 h. Based on previous experiments with the same product, 4 doses of the *S. cerevisiae* preparation were tested as feed additive in batch cultures at 0, 25, 50 and 100 µL/bottle. VFA and gas production, pH, ammonia-N concentrations and true in vitro digestibility (TIVD) were measured. There were no additive x substrate interactions ($P > 0.05$) for any variable. TIVD, ammonia-N concentration and acetate:propionate ratio were not affected ($P > 0.05$) by SC-47 addition to the batch cultures. Gas production and total VFA production were linearly increased ($P < 0.001$) by increasing amounts of SC-47, whereas pH was linearly decreased ($P = 0.010$). Also, the production of all individual VFA linearly increased with the addition of the different doses of SC-47 (acetate, $P = 0.001$; propionate, $P < 0.001$; butyrate, $P < 0.001$; and the sum of isobutyrate, isovalerate and valerate, $P < 0.001$). The results show that *S. cerevisiae* stimulate ruminal fermentation in vitro of these fibrous forages of different quality, and so, studies analyzing their possible influence on fermentation of low-quality substrates are recommended.

Key Words: *Saccharomyces cerevisiae*, batch culture, forage

W432 Nutritional evaluation of corn wet feed in cannulated Nili-Ravi buffalo bulls. M. Nisa*[1], M. Osman[3], S. Najeeb[4], and M. Sarwar[2], *[1]Department of Food Science, Nutrition and Home Economics, Govt. College University, Faisalabad, Pakistan, [2]Institute of Animal Sciences, University of Agriculture, Faisalabad, Pakistan, [3]Livestock and Dairy Development Board, Lahore, Pakistan, [4]Star Farm Pvt Ltd., Sargodha, Pakistan.*

The study was aimed to examine the influence of replacing corn wet feed (CWF) with corn grains on feed intake, nutrient digestibility, nitrogen balance and ruminal characteristics in ruminal cannulated buffalo bulls. The animals were fed 1% of their body weight. All diets were isocaloric (2.30 Mcal/kg) and isonitrogenous (12.55%CP). The control diet CWF0 did not contain CWF, Whereas CWF10, CWF20 and CWF30 diets had 10, 20, and 30% CWF, respectively. Animals were housed on concrete floor in separate pens and water was made available round the clock. The experiment lasted for 80 d. The 4 × 4 Latin square design was used in this experiment and means were compared by Duncan's new multiple range test. Dry matter (DM) and crude protein (CP) intakes were not differ ($P > 0.05$) in animals fed diets containing with and without CWF. Neutral detergent fiber (NDF) intake was higher ($P < 0.05$) in buffalo bulls fed diets contained different levels of CWF. Dry matter, CP and NDF digestibilities were highest ($P < 0.05$) in animals fed CWF10 diet than those fed CWF0, CWF20 and CWF30 diets while DM, CP and NDF digestibilities remained same ($P > 0.05$) among animals groups fed CWF0, CWF20 and CWF30 diets. All animal were in positive nitrogen balance. However, there was high nitrogen retention observed in animal fed CWF10 and CWF20 diets. Ruminal pH in buffalo bulls at 0, 3, 6 and 9 h remained same across all diets. Ruminal NH_3-N at 0 h was also same while significant ($P < 0.05$) difference was observed in buffalo bulls at 3, 6 and 9 h across all diets. In this study 10% replacement of corn grain with CWF showed better nutrient digestibility, nitrogen balance and ruminal characteristics of Nili-Ravi buffalo bulls.

Key Words: corn wet feed, corn replacement, buffalo bulls

W433 Effect of direct-fed microbial supplementation and different diets on performance and carcass characteristics in beef feedlot heifers. Laura F. Prados*[2,1], Galen E. Erickson[1], Nirosh Aluthge[1], Samodha C. Fernando[1], Curtis J. Bittner[1], and Fred H. Hilscher[1], *[1]University of Nebraska-Lincoln, Lincoln, NE, [2]Universidade Federal de Viçosa-MG, Viçosa, Minas Gerais, Brazil.*

The objective of this study was to measure feedlot performance and carcass characteristics of heifers fed a newly developed direct-fed microbial (DFM) or not within 2 different basal diets. Three hundred thirty-six heifers (348 ± 33 kg) were used in a randomized block designed study with 24 pens (6 replications/treatment). The treatment design was a 2 × 2 factorial arrangement consisting of 2 basal diets based on corn (CON) or 40% modified distillers grains plus solubles replacing corn (MDGS) and presence (1×10^9 cfu/mL of each bacteria species/animal per day) or absence of DFM. The DFM was isolated from prior experiments, grown in the lab, and consisted of members of *Bacteroides* and *Lachnospiraceae* that were top-dressed on feed immediately after feeding to ensure accurate supply daily to pens. One block (4 pens) of heifers was harvested after 133 d on feed and 3 blocks (20 pens) were harvested after 147 d on feed. Hot carcass weight was obtained the day of harvest, and LM area and fat thickness collected after a 48-h chill. Carcass adjusted final BW was calculated using HCW divided by a common dressing percentage (63%), and used for ADG and G:F. All data were analyzed using the MIXED procedure of SAS with an $\alpha = 0.05$ and pen as the experimental unit. There were no interactions ($P > 0.25$) between diet and DFM supplementation for DMI, ADG, G:F, and HCW; thus, main effects of basal diet and DFM are presented. There were no differences in DMI, ADG, and carcass characteristics ($P > 0.23$) due to supplementation of DFM. Heifers fed DFM tended ($P = 0.10$) to be less efficient. Feeding MDGS increased ($P < 0.01$) DMI, ADG, and HCW of heifers. Feed efficiency was improved ($P < 0.01$) by 7% for heifers fed MDGS diets compared with CON. Heifers fed MDGS were fatter ($P < 0.01$) compared with CON likely due to greater ADG. The DFM developed for this study did not enhance performance, while feeding modified distillers grains compared with corn improved performance.

Key Words: carcass characteristics, direct-fed microbial, modified distillers grains plus solubles

W434 Effect of Econase on rumen fermentation patterns, diet digestibility and performance pre-and postpartum of primiparous dairy cows. D. N. Lobão da Silva*[1], R. Riewer[2], A. Gander[1], N. Walker[2], B. Ellison[2], M. Endres[1], and N. B. Litherland[1], *[1]University of Minnesota, Saint Paul, MN. USA, [2]AB Vista, Marlborough, UK.*

The objective of this study was to examine the effect of feeding a fibrolytic enzyme preparation (Econase) via a molasses-based liquid feed (MLF) on digestibility, ruminal patterns and milk production of primiparous dairy cows. Thirty-six (n = 18) dairy heifers were blocked by BW, BCS, mature 305 ME and assigned to 2 treatments from d 45 pre- to 56 postpartum: 1) untreated MLF diet (CON); 2) enzyme treated MLF diet (ECO). Treated MLF preparation conferred activity of 3,500